

CLAIM AMENDMENTS

Claims 1 to 27 (canceled)

Claim 28 (Currently Amended)

An isolated nucleic acid ~~specific to mycobacteria of M.tuberculosis complex~~ having a nucleotide sequence selected from the group consisting of SEQ ID No: 1, SEQ ID No: 2, the complement of SEQ ID No: 1, and the complement of SEQ ID No: 2.

Claim 29 (Currently Amended)

An isolated nucleic acid ~~specific to mycobacteria of M.tuberculosis complex~~ having a nucleotide sequence selected from the group consisting of SEQ ID No: 1 and the complement of SEQ ID No: 1.

Claim 30 (Currently Amended)

An isolated nucleic acid ~~specific to mycobacteria of M.tuberculosis complex which mycobacteria is different from BCG, whereas said nucleic acid has~~ having a nucleotide sequence selected from the group consisting of SEQ ID No: 2 and the complement of SEQ ID No: 2.

Claim 31 (Previously Presented)

A cloning or expression vector containing a nucleic acid sequence selected from the group consisting of SEQ ID No: 1, SEQ ID No: 2, the complement of SEQ ID No: 1, and the complement of SEQ ID No: 2.

Claim 32 (previously presented)

A vector of claim 31 which is a plasmid selected from the group consisting of pRegX3Bc1 and pRegX3Mt1 deposited at CNCM under Nos. I-1765 and I-1766, respectively.

Claim 33 (Canceled)

Claim 34 (Previously Presented)

A nucleotide probe or nucleotide primer comprising 24 consecutive nucleotides selected from a sequence selected from the group consisting of SEQ ID No:1, SEQ ID No: 2, the complement of SEQ ID No: 1, and the complement of SEQ ID No: 2.

Claim 35 (Currently Amended)

A nucleotide probe ~~or nucleotide primer that~~ hybridizes at 68°C in a 5xSSC hybridization buffer with one ~~of the sequences~~ comprising a sequence selected from the

group consisting of sequence SEQ ID No: 1, ~~or the~~
complement of SEQ ID No: 1, ~~or their corresponding RNA~~
sequences and their corresponding gene[s], ~~and that~~
~~contains a maximum of 21 base pairs.~~

Claim 36 (Currently Amended)

A nucleotide probe ~~or nucleotide primer that~~
~~hybridizes at 68°C in a 5xSSC hybridization buffer with one~~
~~of the sequences having a sequence comprising two~~
successive sequences SEQ ID No: 1 followed by a sequence
SEQ ID No: 2 ~~or their corresponding RNA sequences or their~~
~~corresponding gene, and that contains a maximum of 21 base~~
~~pairs.~~

Claim 37 (Currently Amended)

A nucleotide probe ~~for detection of specific sequences~~
~~of nucleic acids of M.tuberculosis complex other than BCG~~
~~wherein said probe that~~ consists of 21 base pairs having a
sequence of a region of sequence SEQ ID No: 2 comprising
the GAG codon in positions 40 to 42 or the complement of
said region.

Claim 38 (Currently Amended)

~~A nucleotide probe for detection of specific sequences of nucleic acids of M. tuberculosis complex other than BCG comprising a sequence composed of nucleotides in positions 31 to 51 of SEQ ID No: 2 or the complement of said sequence.~~

Claim 39 (Canceled)

Claim 40 (Currently Amended)

A nucleotide probe ~~of claim 37~~ comprising the sequence SEQ ID No: 2 or the complement of SEQ ID No: 2.

Claim 41 (Currently Amended)

A nucleotide probe ~~or nucleotide primer that hybridizes at 68°C in a 5xSSC hybridization buffer with~~ labeled by digoxigenin comprising one of the sequences selected from the group consisting of SEQ ID No: 1, SEQ ID No: 2, the complement of SEQ ID No: 1, and the complement of SEQ ID No: 2, their corresponding RNA sequences or and their corresponding gene[s], and that contains a maximum of 21 base pairs, which is labeled by digoxigenin.

Claim 42 (Canceled)

Claim 43 (Canceled)

Claim 44 (Currently Amended)

A nucleotide primer pair ~~of claim 42~~ comprising ~~the~~ a pair of primers 5'GCGCGAGAGCCCGAACTGC3' (SEQ ID No: 4) and 5'GCGCAGCAGAAACGTCAGC3' (SEQ ID No: 5).

Claims 45 and 46 (canceled)

Claim 47 (Currently Amended)

A method of detecting a mycobacteria ~~stain~~ strain of M. tuberculosis complex in a biological sample comprising (1) contacting the biological sample to a pair of primers 5'GCGCGAGAGCCCGAACTGC3' (SEQ ID No: 4) and 5'GCGCAGCAGAAACGTCAGC3' (SEQ ID No: 5) wherein ~~one primer comprises the nucleotide sequence of sequences adjacent to the senX3-regX3 region in the 3' of senX3 region and the other primer comprises the nucleotide sequence of sequences adjacent to the senX3-regX3 region in the 5' of regX3 region~~ under conditions to effect hybridization of the primers to a nucleotide sequence ~~the specific nucleic acids~~ of mycobacteria strains of M. tuberculosis complex; (2) effecting amplification of ~~the said~~ nucleotide sequence ~~nucleic acids~~;

(3) contacting the biological sample containing said nucleotide sequences amplified from step (2) with a nucleotide probe ~~that hybridizes at 68°C in a 5xSSC hybridization buffer with one of the sequences that comprises a sequence selected from the group consisting of SEQ ID No: 1, or sequence SEQ ID No: 2, or the complement of SEQ ID No: 1, or and the complement of SEQ ID No: 2, or one of their corresponding RNA sequences or one of their corresponding gene[s], or a sequence of two successive sequence of SEQ ID No: 1 followed by SEQ ID No: 2, and that contains a maximum of 21 base pairs under conditions for formation of hybridization complexes between the said probe and said nucleotide sequences amplified sequences from step (2) of nucleic acids;~~ and

(4) detecting if any hybridization complexes are present, which complexes indicate ~~the a~~ presence of a mycobacteria strain of *M. tuberculosis* complex.

Claim 48 (Canceled)

Claim 49 (Currently Amended)

The method of claim 47 wherein the nucleotide probe comprises ~~a region of SEQ ID No: 2 comprising the GAG codon in positions 40 to 42 or the complement of said region a~~

sequence composed of nucleotides in positions 31 to 51 of
SEQ ID No: 2 or the complement of said sequence.

Claim 50 (previously presented)

The method of claim 49 effected upon immunodeficient humans to differentiate an infection by BCG from an infection by a virulent mycobacterium of M. tuberculosis complex.

Claim 51 (previously presented)

The method of claim 50 wherein the human is infected with HIV.

Claim 52 (Currently Amended)

A method of identifying groups of mycobacteria belonging to a M. tuberculosis complex comprising

(1) contacting ~~the a~~ DNA of previously extracted strains of the M. tuberculosis complex with a nucleotide primer pair comprising a pair of primers
5'GCGCGAGAGCCCGAACTGC3' (SEQ ID No: 4) and
5'GCGCAGCAGAAACGTCAGC3' (SEQ ID No: 5)~~-of claims 35 and 42~~
under conditions permitting a specific hybridization of the primers respectively 56 base pairs upstream and 62 base
pairs downstream of ~~with one of the sequences of claim 28~~

a sequence selected from the group consisting of SEQ ID No: 1, SEQ ID No: 2, the complement of SEQ ID No: 1 and the complement of SEQ ID No: 2, to obtain amplification products and

(2) measuring ~~the~~a length of the amplification products obtained from step (1).

Claim 53 (Canceled)

Claim 54 (Currently Amended)

A kit for in vitro identification of strains of mycobacteria of a ~~the~~-M. tuberculosis complex in a biological sample comprising (1) ~~a primer pair for amplification of a specific nucleotide sequence of mycobacteria of M. tuberculosis complex, one primer consisting of the nucleotide sequence of sequences adjacent to the senX3-regX3 region in the 3' of senX3 region and the other primer consisting of the nucleotide sequence of sequences adjacent to the senX3-regX3 region in the 5' of regX3 region~~ a pair of primers 5'GCGCGAGAGCCCGAACTGC3' (SEQ ID No: 4) and 5'GCGCAGCAGAAACGTCAGC3' (SEQ ID No: 5).

Claim 55 (Currently Amended)

A method of detection and of differential diagnosis of BCG and the members of *M. tuberculosis* complex in a biological sample comprising:

(1) contacting the biological sample to a nucleotide primer pair comprising a pair of primers 5'GCGCGAGAGCCCGAACTGC3' (SEQ ID No: 4) and 5'GCGCAGCAGAAACGTCAGC3' (SEQ ID No: 5) for amplification of a ~~specific~~-nucleotide sequence of mycobacteria of *M. tuberculosis* complex, ~~one primer comprising the nucleotide sequence of sequences adjacent to the senX3-regX3 region in the 3' of senX3 region and the other primer comprising the nucleotide sequence of sequences adjacent to the senX3-regX3 region in the 5' of regX3 region~~ under conditions to effect hybridization of the primers to said nucleotide sequence ~~the specific nucleic acids~~ of mycobacteria strains of *M. tuberculosis* complex;

(2) effecting amplification of ~~the~~ said nucleotide sequence ~~nucleic acids~~;

(3) contacting the biological sample containing said nucleotide sequence amplified from step (2) with a nucleotide probe of two successive sequences SEQ ID No: 1 followed by a sequence SEQ ID No: 2 under conditions for formation of hybridization complexes between ~~the~~ said probe

and said nucleotide amplified sequences amplified from step
(2) ~~of nucleic acids;~~

(4) detecting any first hybridization complexes
present; and

(5) determining if said first hybridization complexes
are also capable of forming second hybridization complexes
with a nucleotide probe for detection of ~~specific~~ sequences
of nucleic acids of M. tuberculosis complex other than BCG
comprising a ~~region of sequence SEQ ID No: 2 comprising the~~
~~GAC codon in positions 40 to 42~~ sequence composed of
nucleotides in positions 31 to 51 of SEQ ID No:2, or the
complement of said sequence region, ~~the~~a presence of said
second hybridization complexes being indicative of ~~the~~a
presence of a M. tuberculosis strain different from BCG and
~~the~~a presence of said first hybridization complexes
uniquely being indicative of the BCG.